

SEQUENCE LISTING

<110> Novo Nordisk A/S

<120> Novel Proteases And Variants Thereof

<130> 5665.204-WO

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<150> PA 1999 01212

<151> 1999-08-31

<150> PA 1999 01500

<151> 1999-10-20

<160> 45

<170> PatentIn Ver. 2.1

<210> 1

<211> 948

<212> DNA

<213> Bacillus licheniformis

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<223> pro_peptide (94) ... (282)

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ggt	att	tct	att	tat	tct	tta	ggt	atg	cac	ccg	gcc	caa	gcc	gcg	cca	96
Gly	Ile	Ser	Ile	Tyr	Ser	Leu	Gly	Met	His	Pro	Ala	Gln	Ala	Ala	Pro	
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tcg	cct	cat	act	cct	ggt	tca	agc	gat	cct	tca	tac	aaa	gcg	gaa	aca	144
Ser	Pro	His	Thr	Pro	Val	Ser	Ser	Asp	Pro	Ser	Tyr	Lys	Ala	Glu	Thr	
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tcg	ggt	act	tat	gac	cca	cac	att	aag	agc	gat	caa	tac	ggc	ttg	tat	192
Ser	Val	Thr	Tyr	Asp	Pro	His	Ile	Lys	Ser	Asp	Gln	Tyr	Gly	Leu	Tyr	
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tca	aaa	gcg	ttt	aca	ggc	acc	ggc	aaa	gtg	aat	gaa	aca	aag	gaa	aaa	240
Ser	Lys	Ala	Phe	Thr	Gly	Thr	Gly	Lys	Val	Asn	Glu	Thr	Lys	Glu	Lys	
	-30				-25				-20					-15		

gcg	gaa	aaa	aag	tca	ccc	gcc	aaa	gct	cct	tac	agc	att	aaa	tcg	gtg	288
Ala	Glu	Lys	Lys	Ser	Pro	Ala	Lys	Ala	Pro	Tyr	Ser	Ile	Lys	Ser	Val	
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Sub B1

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Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro	
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tac aga gcg atc gtt cat att tca agc agc atc ggt tca tgc acc gga	384
Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly	
20 25 30	
tgg atg atc ggt ccg aaa acc gtc gca aca gcc gga cac tgc atc tat	432
Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr	
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gac aca tca agc ggt tca ttt gcc ggt aca gcc act gtt tgc ccg gga	480
Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly	
55 60 65	
cgg aac ggg aca agc tat cct tac ggc tca gtt aaa tgc acg cgc tac	528
Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr	
70 75 80	
ttt att ccg tca gga tgg aga agc gga aac acc aat tac gat tac gga	576
Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly	
85 90 95	
gca atc gaa cta agc gaa ccg atc ggc aat act gtc gga tac ttc gga	624
Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly	
100 105 110	
tac tgc tac act act tca tca ctt gtt ggg aca act gtt acc atc agc	672
Tyr Ser Tyr Thr Thr Ser Leu Val Gly Thr Thr Val Thr Ile Ser	
115 120 125 130	
ggc tac cca ggc gat aaa aca gca ggc aca caa tgg cag cat tca gga	720
Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly	
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ccg att gcc atc tcc gaa acg tat aaa ttg cag tac gca atg gac acg	768
Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr	
150 155 160	
tac gga gga caa agc ggt tca ccg gta ttc gaa caa agc agc tcc aga	816
Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg	
165 170 175	
acg aac tgt agc ggt ccg tgc tgc ctt gcc gta cac aca aat gga gta	864
Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val	
180 185 190	
tac ggc ggc tcc tgc tac aac aga ggc acc ccg att aca aaa gag gtg	912
Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val	
195 200 205 210	
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 Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr
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 Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys
 -30 -25 -20 -15
 Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val
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 Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly
 20 25 30
 Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr
 35 40 45 50
 Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly
 55 60 65
 Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr
 70 75 80
 Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly
 85 90 95
 Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly
 100 105 110
 Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser
 115 120 125 130
 Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly
 135 140 145
 Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr
 150 155 160
 Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg
 165 170 175
 Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val
 180 185 190
 Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val
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 Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
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11-1-81
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ggg att cta tcc cca gta aac gca act caa gct gag act ctt act aaa 96
Gly Ile Leu Ser Pro Val Asn Ala Thr Gln Ala Glu Thr Leu Thr Lys
-100 -95 -90

tta aat aaa ata agt cag aag cag gaa cca tca tat aaa cta gat gaa 144
Leu Asn Lys Ile Ser Gln Lys Gln Glu Pro Ser Tyr Lys Leu Asp Glu
-85 -80 -75

gaa atg gat tat gtt cta att gat ttg gaa aca caa tct gaa tcg att 192
Glu Met Asp Tyr Val Leu Ile Asp Leu Glu Thr Gln Ser Glu Ser Ile
-70 -65 -60

att tcg ata gga gat aat acc gat ttg gga gat caa tcg ttt act tct 240
Ile Ser Ile Gly Asp Asn Thr Asp Leu Gly Asp Gln Ser Phe Thr Ser
-55 -50 -45

tta ggg aag gtg gga cat gga gaa ctt gag aaa att aac tta gaa gaa 288
Leu Gly Lys Val Gly His Gly Glu Leu Glu Lys Ile Asn Leu Glu Glu
-40 -35 -30 -25

ttt cgt aat cct aat tta aca gta gta gac ccg tta aca cgt aag cct 336
Phe Arg Asn Pro Asn Leu Thr Val Val Asp Pro Leu Thr Arg Lys Pro
-20 -15 -10

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Ile Glu Gln Lys Ile Ser Pro Phe Val Val Ile Gly Asp Asp Gly Arg
-5 -1 1 5

aga caa gtt caa aat act tct ttc atg cca ttt cgt gca ctt act tat 432
Arg Gln Val Gln Asn Thr Ser Phe Met Pro Phe Arg Ala Leu Thr Tyr
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att gag ttt gga aac ctt aca agt aca tgg agt tgt tct gga ggt gtg 480
Ile Glu Phe Gly Asn Leu Thr Ser Thr Trp Ser Cys Ser Gly Gly Val
25 30 35 40

att gga aca gat tta gtt gtt act aat gca cat tgt gta gaa ggt tct 528
Ile Gly Thr Asp Leu Val Val Thr Asn Ala His Cys Val Glu Gly Ser
45 50 55

gtg tta gca ggt act gta gtt cct ggt atg aac aat agt cag tgg gca 576
Val Leu Ala Gly Thr Val Val Pro Gly Met Asn Asn Ser Gln Trp Ala
60 65 70

tat ggg cat tat agg gtt act cag att atc tac cct gat caa tac aga 624
Tyr Gly His Tyr Arg Val Thr Gln Ile Ile Tyr Pro Asp Gln Tyr Arg
75 80 85

aat aac ggt gct tca gag ttt gat tat gct ata ctt aga gta gca cct 672

Rub 31

Asn	Asn	Gly	Ala	Ser	Glu	Phe	Asp	Tyr	Ala	Ile	Leu	Arg	Val	Ala	Pro	
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gac	tct	gat	gga	cgt	cat	att	gga	aac	aga	gct	gga	att	tta	tct	ttt	720
Asp	Ser	Asp	Gly	Arg	His	Ile	Gly	Asn	Arg	Ala	Gly	Ile	Leu	Ser	Phe	
105					110					115					120	
aca	gaa	aca	gga	act	gtt	aac	gaa	aat	act	ttt	cta	aga	acg	tat	gga	768
Thr	Glu	Thr	Gly	Thr	Val	Asn	Glu	Asn	Thr	Phe	Leu	Arg	Thr	Tyr	Gly	
				125					130					135		
tac	ccc	ggt	gat	aaa	ata	tca	gag	aca	aaa	tta	att	tct	ttg	tgg	gga	816
Tyr	Pro	Gly	Asp	Lys	Ile	Ser	Glu	Thr	Lys	Leu	Ile	Ser	Leu	Trp	Gly	
			140					145					150			
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Met	Val	Gly	Arg	Ser	Asp	Ala	Phe	Leu	His	Arg	Asp	Leu	Leu	Phe	Tyr	
		155				160						165				
aat	atg	gac	acc	tat	ttt	ggt	caa	tca	ggt	tct	cct	gta	tta	aac	agc	912
Asn	Met	Asp	Thr	Tyr	Phe	Gly	Gln	Ser	Gly	Ser	Pro	Val	Leu	Asn	Ser	
	170					175					180					
gta	gat	tca	atg	gtt	gcg	gtt	cat	aat	gca	ggg	tat	atc	gtt	ggt	ggt	960
Val	Asp	Ser	Met	Val	Ala	Val	His	Asn	Ala	Gly	Tyr	Ile	Val	Gly	Gly	
	185				190					195				200		
aat	agg	gaa	att	aat	ggt	ggt	cct	aaa	atc	aga	aga	gat	ttt	aca	aac	1008
Asn	Arg	Glu	Ile	Asn	Gly	Gly	Pro	Lys	Ile	Arg	Arg	Asp	Phe	Thr	Asn	
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Leu	Phe	Asn	Gln	Met	Asn											
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Gly	Ile	Leu	Ser	Pro	Val	Asn	Ala	Thr	Gln	Ala	Glu	Thr	Leu	Thr	Lys	
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Leu	Asn	Lys	Ile	Ser	Gln	Lys	Gln	Glu	Pro	Ser	Tyr	Lys	Leu	Asp	Glu	
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Ile	Ser	Ile	Gly	Asp	Asn	Thr	Asp	Leu	Gly	Asp	Gln	Ser	Phe	Thr	Ser	
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Phe	Arg	Asn	Pro	Asn	Leu	Thr	Val	Val	Asp	Pro	Leu	Thr	Arg	Lys	Pro	
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Arg	Gln	Val	Gln	Asn	Thr	Ser	Phe	Met	Pro	Phe	Arg	Ala	Leu	Thr	Tyr
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Ile	Gly	Thr	Asp	Leu	Val	Val	Thr	Asn	Ala	His	Cys	Val	Glu	Gly	Ser
				45					50					55	
Val	Leu	Ala	Gly	Thr	Val	Val	Pro	Gly	Met	Asn	Asn	Ser	Gln	Trp	Ala
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Tyr	Gly	His	Tyr	Arg	Val	Thr	Gln	Ile	Ile	Tyr	Pro	Asp	Gln	Tyr	Arg
		75					80					85			
Asn	Asn	Gly	Ala	Ser	Glu	Phe	Asp	Tyr	Ala	Ile	Leu	Arg	Val	Ala	Pro
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Asp	Ser	Asp	Gly	Arg	His	Ile	Gly	Asn	Arg	Ala	Gly	Ile	Leu	Ser	Phe
105					110					115					120
Thr	Glu	Thr	Gly	Thr	Val	Asn	Glu	Asn	Thr	Phe	Leu	Arg	Thr	Tyr	Gly
				125					130						135
Tyr	Pro	Gly	Asp	Lys	Ile	Ser	Glu	Thr	Lys	Leu	Ile	Ser	Leu	Trp	Gly
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Asn	Met	Asp	Thr	Tyr	Phe	Gly	Gln	Ser	Gly	Ser	Pro	Val	Leu	Asn	Ser
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Val	Asp	Ser	Met	Val	Ala	Val	His	Asn	Ala	Gly	Tyr	Ile	Val	Gly	Gly
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Asn	Arg	Glu	Ile	Asn	Gly	Gly	Pro	Lys	Ile	Arg	Arg	Asp	Phe	Thr	Asn
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48

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 Ile Ser Ile Phe Ser Ser Gly Ile Tyr Ser Ala Gln Ala Ala Ser Ser
 -75 -70 -65
 ccg cat acc cca gtc tcc agc gac cct tcg tac aag ccc ggc tcc acc 144
 Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Gly Ser Thr
 -60 -55 -50 -45
 tat gat ccc aac ata aaa att gac aat aac ggc gca tat tcg aaa gcc 192
 Tyr Asp Pro Asn Ile Lys Ile Asp Asn Asn Gly Ala Tyr Ser Lys Ala
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 Phe Glu Gly Thr Gly Thr Pro Gly Gly Ser Val Gln Ala Lys Pro Lys
 -25 -20 -15
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 Lys Glu Ser Pro Ala Gly Pro Pro Tyr Ser Pro Lys Ser Val Ile Gly
 -10 -5 -1 1
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 Ser Asp Glu Arg Thr Arg Val Thr Asp Thr Thr Ala Phe Pro Tyr Arg
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 Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly Trp Leu
 25 30 35
 atc gga ccg aaa acg gta gca acg gcc ggc cac tgc gtc tat gac acg 432
 Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Val Tyr Asp Thr
 40 45 50
 gca agc cga tca ttc gcg gga acc gcc acc gtt tcc ccg gga cga aac 480
 Ala Ser Arg Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly Arg Asn
 55 60 65
 ggt tca gct tac cct tac gga tct gtt aca tcg acc cgc tat ttc atc 528
 Gly Ser Ala Tyr Pro Tyr Gly Ser Val Thr Ser Thr Arg Tyr Phe Ile
 70 75 80
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 Pro Ser Gly Trp Gln Ser Gly Asn Ser Asn Tyr Asp Tyr Ala Ala Ile
 85 90 95 100
 gag ctc agc cag ccg atc ggc aat acc gtc gga tat ttc gga tat tca 624
 Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly Tyr Ser
 105 110 115
 tac acc gct tca tcg ctt gca gga gca ggc gtg acc atc agc gga tat 672
 Tyr Thr Ala Ser Ser Leu Ala Gly Ala Gly Val Thr Ile Ser Gly Tyr
 120 125 130
 cca gga gac aaa aca aca ggc acc cag tgg caa atg tcc gga acg atc 720
 Pro Gly Asp Lys Thr Thr Gly Thr Gln Trp Gln Met Ser Gly Thr Ile
 135 140 145
 gct gtt tca gaa acg tat aaa ctg caa tat gcg atc gac aca tac gga 768
 Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile Asp Thr Tyr Gly
 150 155 160
 ggt caa agc ggt tcc ccg gta tat gag aaa agc agt tca agg aca aac 816
 Gly Gln Ser Gly Ser Pro Val Tyr Glu Lys Ser Ser Ser Arg Thr Asn
 165 170 175 180
 tgc agc ggc cca tgc tcg ctg gcc gtt cat acg aac ggc gtg tac gga 864

Ref-B1

Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val Tyr Gly
185 190 195
gga tcc tct tac aac aga ggc acc cgc att acg aaa gaa gta ttt gat 912
Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val Phe Asp
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aat ttc aca agc tgg aaa aac agc gca cag 942
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Phe Glu Gly Thr Gly Thr Pro Gly Gly Ser Val Gln Ala Lys Pro Lys
-25 -20 -15
Lys Glu Ser Pro Ala Gly Pro Pro Tyr Ser Pro Lys Ser Val Ile Gly
-10 -5 -1 1
Ser Asp Glu Arg Thr Arg Val Thr Asp Thr Thr Ala Phe Pro Tyr Arg
5 10 15 20
Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly Trp Leu
25 30 35
Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Val Tyr Asp Thr
40 45 50
Ala Ser Arg Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly Arg Asn
55 60 65
Gly Ser Ala Tyr Pro Tyr Gly Ser Val Thr Ser Thr Arg Tyr Phe Ile
70 75 80
Pro Ser Gly Trp Gln Ser Gly Asn Ser Asn Tyr Asp Tyr Ala Ala Ile
85 90 95 100
Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly Tyr Ser
105 110 115
Tyr Thr Ala Ser Ser Leu Ala Gly Ala Gly Val Thr Ile Ser Gly Tyr
120 125 130
Pro Gly Asp Lys Thr Thr Gly Thr Gln Trp Gln Met Ser Gly Thr Ile
135 140 145
Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile Asp Thr Tyr Gly
150 155 160

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Gly Gln Ser Gly Ser Pro Val Tyr Glu Lys Ser Ser Ser Arg Thr Asn
165 170 175 180
Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val Tyr Gly
185 190 195
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Asn Phe Thr Ser Trp Lys Asn Ser Ala Gln
215 220

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gct tta agt gtg cct agt ttt gcc cat gcc gca tct gat tca gtg cta 96
Ala Leu Ser Val Pro Ser Phe Ala His Ala Ala Ser Asp Ser Val Leu
-70 -65 -60
acg tct gat tat gac atg gtg act tct gat gga aag gtg atc tct tca 144
Thr Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser
-55 -50 -45
agt gat ttc cac aat gat acg aaa tcc ccc tca tcc ttt gat aaa gtg 192
Ser Asp Phe His Asn Asp Thr Lys Ser Pro Ser Ser Phe Asp Lys Val
-40 -35 -30 -25
gat gat cta tct tca act gtt ggt gaa aaa gta aaa cca cta tca aaa 240
Asp Asp Leu Ser Ser Thr Val Gly Glu Lys Val Lys Pro Leu Ser Lys
-20 -15 -10
tat tta aaa gac ttt caa aca aaa gtc gtc att gga gac gat ggt aga 288
Tyr Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg
-5 -1 1 5
aca aaa gta gca aat aca aga gtg gca cca tat aat tca att gct tat 336
Thr Lys Val Ala Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr
10 15 20
act acg ttt ggc ggc tcc agc tgc acg ggg acc ctg att gcc cct aac 384
Thr Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn
25 30 35 40
aaa att ttg aca aac gga cac tgc gtg tac aat aca gca tcc aga agt 432

Del B1

Lys	Ile	Leu	Thr	Asn	Gly	His	Cys	Val	Tyr	Asn	Thr	Ala	Ser	Arg	Ser	
				45					50					55		
tat	agt	gca	aaa	gga	tcg	gtg	tat	cca	ggc	atg	aat	gat	agt	act	gcg	480
Tyr	Ser	Ala	Lys	Gly	Ser	Val	Tyr	Pro	Gly	Met	Asn	Asp	Ser	Thr	Ala	
			60					65					70			
gtg	aat	ggc	tca	gca	aat	atg	aca	gag	ttc	tat	gta	cca	agc	ggg	tat	528
Val	Asn	Gly	Ser	Ala	Asn	Met	Thr	Glu	Phe	Tyr	Val	Pro	Ser	Gly	Tyr	
			75				80					85				
atc	aat	aca	ggg	gca	agc	caa	tat	gat	ttt	gcc	gtg	atc	aaa	aca	gat	576
Ile	Asn	Thr	Gly	Ala	Ser	Gln	Tyr	Asp	Phe	Ala	Val	Ile	Lys	Thr	Asp	
			90			95					100					
acg	aac	att	ggc	aat	aca	gtt	ggg	tac	cgt	tcc	atc	cgt	cag	gtg	aca	624
Thr	Asn	Ile	Gly	Asn	Thr	Val	Gly	Tyr	Arg	Ser	Ile	Arg	Gln	Val	Thr	
			105			110				115					120	
aac	tta	act	ggg	aca	acg	att	aaa	att	tct	gga	tat	cca	ggg	gat	aaa	672
Asn	Leu	Thr	Gly	Thr	Thr	Ile	Lys	Ile	Ser	Gly	Tyr	Pro	Gly	Asp	Lys	
				125					130					135		
atg	aga	tca	act	ggc	aag	atc	tcg	cag	tgg	gag	atg	tca	ggg	cct	gtg	720
Met	Arg	Ser	Thr	Gly	Lys	Ile	Ser	Gln	Trp	Glu	Met	Ser	Gly	Pro	Val	
				140				145					150			
aca	aga	gaa	gat	acg	aat	ctc	gca	tac	tat	atg	att	gat	aca	ttt	agt	768
Thr	Arg	Glu	Asp	Thr	Asn	Leu	Ala	Tyr	Tyr	Met	Ile	Asp	Thr	Phe	Ser	
			155				160					165				
gga	aat	tca	ggc	tca	gca	atg	cta	gat	caa	aat	cag	caa	att	gtt	ggg	816
Gly	Asn	Ser	Gly	Ser	Ala	Met	Leu	Asp	Gln	Asn	Gln	Gln	Ile	Val	Gly	
			170			175					180					
gtt	cat	aac	gca	ggg	tat	tca	aac	ggg	acg	att	aat	ggc	ggg	cca	aaa	864
Val	His	Asn	Ala	Gly	Tyr	Ser	Asn	Gly	Thr	Ile	Asn	Gly	Gly	Pro	Lys	
					190				195						200	
gcg	aca	gct	gcc	ttt	gtt	gaa	ttt	atc	aac	tat	gca	aaa	gcg	caa		909
Ala	Thr	Ala	Ala	Phe	Val	Glu	Phe	Ile	Asn	Tyr	Ala	Lys	Ala	Gln		
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 <212> PRT
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 -85 -80 -75
 Ala Leu Ser Val Pro Ser Phe Ala His Ala Ala Ser Asp Ser Val Leu
 -70 -65 -60
 Thr Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser
 -55 -50 -45
 Ser Asp Phe His Asn Asp Thr Lys Ser Pro Ser Ser Phe Asp Lys Val
 -40 -35 -30 -25
 Asp Asp Leu Ser Ser Thr Val Gly Glu Lys Val Lys Pro Leu Ser Lys
 -20 -15 -10
 Tyr Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg

[illegible]

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Met Lys Lys Ser Val Thr Arg Val Leu Met Ala Gly Leu Ile Gly Ile
-95 -90 -85

22-11-81

tct att tat tct atg ggc atc gac tcc gct caa gct gca tca tcc ccg	96
Ser Ile Tyr Ser Met Gly Ile Asp Ser Ala Gln Ala Ala Ser Ser Pro	
-80 -75 -70 -65	
cat act cct gtc tct agc gat cct tca tac aag ccc gac tca tcc gca	144
His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Asp Ser Ser Ala	
-60 -55 -50	
agc tat gat cct gct att aaa acc aac aaa aac ggc gcc tat tca aaa	192
Ser Tyr Asp Pro Ala Ile Lys Thr Asn Lys Asn Gly Ala Tyr Ser Lys	
-45 -40 -35	
gca ttt gaa ggt aca gga aaa cta gac gct ccc ctt tat cag gaa aaa	240
Ala Phe Glu Gly Thr Gly Lys Leu Asp Ala Pro Leu Tyr Gln Glu Lys	
-30 -25 -20	
agc aaa cca acc aaa aaa tcc cct gcc gga cca cgt tac agc ccc aaa	288
Ser Lys Pro Thr Lys Lys Ser Pro Ala Gly Pro Arg Tyr Ser Pro Lys	
-15 -10 -5 -1	
tcc gtg att ggt tct gat gaa cgg acg aga gtg aca aac act acc gca	336
Ser Val Ile Gly Ser Asp Glu Arg Thr Arg Val Thr Asn Thr Thr Ala	
1 5 10 15	
tat cca tac aga gcg atc gtg cat att tca agc agc atc ggg tct tgc	384
Tyr Pro Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys	
20 25 30	
acc ggc tcc ctg atc ggt ccg aaa acg gtg gca acg gcc gga cac tgc	432
Thr Gly Ser Leu Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys	
35 40 45	
att tat gac aca gcg agc ggg tca ttc gcc gga acc gct acc gtt tct	480
Ile Tyr Asp Thr Ala Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser	
50 55 60	
ccg gga cgg aac ggt tca aca tat ccg tac gga tca gtt aca tca acc	528
Pro Gly Arg Asn Gly Ser Thr Tyr Pro Tyr Gly Ser Val Thr Ser Thr	
65 70 75 80	
cgc tat ttc atc ccg tca ggc tat cga agc gga aat tcc aat tac gac	576
Arg Tyr Phe Ile Pro Ser Gly Tyr Arg Ser Gly Asn Ser Asn Tyr Asp	
85 90 95	
tac gga gcc ata gag ctc agc cag ccg atc ggc aac acc gtc ggg tat	624
Tyr Gly Ala Ile Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr	
100 105 110	
ttc gga tat tcc tac acc acc tcc tct ctc gtt ggg tca agc gtt acc	672
Phe Gly Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Ser Ser Val Thr	
115 120 125	
atc atc gga tat cca ggc gac aaa aca tcc ggc acc caa tgg cag atg	720
Ile Ile Gly Tyr Pro Gly Asp Lys Thr Ser Gly Thr Gln Trp Gln Met	
130 135 140	
tcc gga aat atc gcc gtc tca gaa aca tat aaa ctg caa tat gcg atc	768
Ser Gly Asn Ile Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile	
145 150 155 160	
gac aca tac gga ggg cag agc ggc tct ccc gta tat gag gcg agc agc	816
Asp Thr Tyr Gly Gly Gln Ser Gly Ser Pro Val Tyr Glu Ala Ser Ser	
165 170 175	
tcc aga acg aat tgc agc ggc cca tgt tcc ctg gcc gtt cat acg aat	864
Ser Arg Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn	

151

180 185 190
ggg gtg tac gga gga tct tca tac aac aga ggc acc cgg att aca aaa 912
Gly Val Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys
195 200 205
gaa gta ttc gat aat ttg aca aac tgg aaa aac agc gcc caa 954
Glu Val Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
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-80 -75 -70 -65
His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Asp Ser Ser Ala
-60 -55 -50
Ser Tyr Asp Pro Ala Ile Lys Thr Asn Lys Asn Gly Ala Tyr Ser Lys
-45 -40 -35
Ala Phe Glu Gly Thr Gly Lys Leu Asp Ala Pro Leu Tyr Gln Glu Lys
-30 -25 -20
Ser Lys Pro Thr Lys Lys Ser Pro Ala Gly Pro Arg Tyr Ser Pro Lys
-15 -10 -5 -1
Ser Val Ile Gly Ser Asp Glu Arg Thr Arg Val Thr Asn Thr Thr Ala
1 5 10 15
Tyr Pro Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys
20 25 30
Thr Gly Ser Leu Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys
35 40 45
Ile Tyr Asp Thr Ala Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser
50 55 60
Pro Gly Arg Asn Gly Ser Thr Tyr Pro Tyr Gly Ser Val Thr Ser Thr
65 70 75 80
Arg Tyr Phe Ile Pro Ser Gly Tyr Arg Ser Gly Asn Ser Asn Tyr Asp
85 90 95
Tyr Gly Ala Ile Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr
100 105 110
Phe Gly Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Ser Ser Val Thr
115 120 125
Ile Ile Gly Tyr Pro Gly Asp Lys Thr Ser Gly Thr Gln Trp Gln Met
130 135 140
Ser Gly Asn Ile Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile
145 150 155 160
Asp Thr Tyr Gly Gly Gln Ser Gly Ser Pro Val Tyr Glu Ala Ser Ser

But 121

				165						170						175			
Ser	Arg	Thr	Asn	Cys	Ser	Gly	Pro	Cys	Ser	Leu	Ala	Val	His	Thr	Asn				
			180					185					190						
Gly	Val	Tyr	Gly	Gly	Ser	Ser	Tyr	Asn	Arg	Gly	Thr	Arg	Ile	Thr	Lys				
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Glu	Val	Phe	Asp	Asn	Leu	Thr	Asn	Trp	Lys	Asn	Ser	Ala	Gln						
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 <223> pro-peptide (76) ... (261)

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		-85					-80					-75				
tta	agt	gtg	cct	agt	ttt	gcc	cat	gca	gca	tct	gat	tca	gta	ctt	acg	96
Leu	Ser	Val	Pro	Ser	Phe	Ala	His	Ala	Ala	Ser	Asp	Ser	Val	Leu	Thr	
	-70					-65					-60					
tct	gat	tat	gac	atg	gtg	act	tct	gac	gga	aag	gtg	att	tct	tca	gct	144
Ser	Asp	Tyr	Asp	Met	Val	Thr	Ser	Asp	Gly	Lys	Val	Ile	Ser	Ser	Ala	
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gac	ttc	cac	aac	gat	atg	aaa	acc	ccc	tca	tcc	ttt	gac	aaa	gtg	gat	192
Asp	Phe	His	Asn	Asp	Met	Lys	Thr	Pro	Ser	Ser	Phe	Asp	Lys	Val	Asp	
			-35					-30						-25		
gat	ctc	tct	tct	act	att	ggc	gaa	aaa	gta	aaa	cca	ctc	aca	aca	tat	240
Asp	Leu	Ser	Ser	Thr	Ile	Gly	Glu	Lys	Val	Lys	Pro	Leu	Thr	Thr	Tyr	
	-20						-15						-10			
tta	aaa	gac	ttt	caa	aca	aaa	gta	gtc	att	gga	gac	gat	ggt	aga	aca	288
Leu	Lys	Asp	Phe	Gln	Thr	Lys	Val	Val	Ile	Gly	Asp	Asp	Gly	Arg	Thr	
	-5					-1	1			5						
aaa	gtg	acg	aat	aca	aga	gta	gca	ccc	tat	aat	tct	att	gct	tat	att	336
Lys	Val	Thr	Asn	Thr	Arg	Val	Ala	Pro	Tyr	Asn	Ser	Ile	Ala	Tyr	Ile	
10				15					20				25			
aca	ttt	ggt	gga	tct	agc	tgc	act	gga	aca	ctc	att	gct	cca	aac	aaa	384
Thr	Phe	Gly	Gly	Ser	Ser	Cys	Thr	Gly	Thr	Leu	Ile	Ala	Pro	Asn	Lys	
				30				35					40			
ata	ttg	aca	aac	gga	cac	tgc	gtc	tac	aat	aca	gcc	aca	aga	agt	tat	432
Ile	Leu	Thr	Asn	Gly	His	Cys	Val	Tyr	Asn	Thr	Ala	Thr	Arg	Ser	Tyr	

Rev B1

			45					50						55				
agt	gca	aaa	ggg	tct	gtc	tac	cca	ggc	atg	aat	gac	agc	acg	gct	gtg			480
Ser	Ala	Lys	Gly	Ser	Val	Tyr	Pro	Gly	Met	Asn	Asp	Ser	Thr	Ala	Val			
		60					65				70							
aac	ggc	tca	gca	aac	atg	acc	gaa	ttc	tat	gta	cca	agc	gga	tat	atc			528
Asn	Gly	Ser	Ala	Asn	Met	Thr	Glu	Phe	Tyr	Val	Pro	Ser	Gly	Tyr	Ile			
	75					80					85							
aac	acg	ggg	gcg	agt	caa	tat	gat	ttt	gcc	gtc	att	aaa	aca	gat	acg			576
Asn	Thr	Gly	Ala	Ser	Gln	Tyr	Asp	Phe	Ala	Val	Ile	Lys	Thr	Asp	Thr			
	90				95					100					105			
aac	att	gga	aat	acg	gtc	ggc	tat	cgc	tct	att	cgt	caa	gtg	aca	aat			624
Asn	Ile	Gly	Asn	Thr	Val	Gly	Tyr	Arg	Ser	Ile	Arg	Gln	Val	Thr	Asn			
				110				115						120				
cta	aca	ggg	aca	acg	att	aaa	att	tct	gga	tat	cca	ggg	gat	aaa	atg			672
Leu	Thr	Gly	Thr	Thr	Ile	Lys	Ile	Ser	Gly	Tyr	Pro	Gly	Asp	Lys	Met			
			125					130					135					
aga	tcg	act	ggc	aaa	gtg	tca	caa	tgg	gaa	atg	tca	ggg	cca	gtc	acg			720
Arg	Ser	Thr	Gly	Lys	Val	Ser	Gln	Trp	Glu	Met	Ser	Gly	Pro	Val	Thr			
	140						145					150						
aga	gaa	gat	acg	aat	ctc	gca	tac	tat	acg	atc	gat	aca	ttt	agc	gga			768
Arg	Glu	Asp	Thr	Asn	Leu	Ala	Tyr	Tyr	Thr	Ile	Asp	Thr	Phe	Ser	Gly			
	155					160					165							
aac	tct	ggc	tct	gcg	atg	cta	gat	caa	aac	caa	caa	atc	gtc	ggg	gtc			816
Asn	Ser	Gly	Ser	Ala	Met	Leu	Asp	Gln	Asn	Gln	Gln	Ile	Val	Gly	Val			
	170				175					180					185			
cat	aat	gcg	ggg	tat	tca	aat	gga	acg	atc	aac	ggg	gga	cca	aaa	gcg			864
His	Asn	Ala	Gly	Tyr	Ser	Asn	Gly	Thr	Ile	Asn	Gly	Gly	Pro	Lys	Ala			
			190					195						200				
act	gct	gcc	ttt	gtt	gaa	ttt	atc	aac	tat	gcg	aag	gcg	caa					906
Thr	Ala	Ala	Phe	Val	Glu	Phe	Ile	Asn	Tyr	Ala	Lys	Ala	Gln					
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 <213> Bacillus pumilus JA96

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Leu	Ser	Val	Pro	Ser	Phe	Ala	His	Ala	Ala	Ser	Asp	Ser	Val	Leu	Thr			
	-70					-65					-60							
Ser	Asp	Tyr	Asp	Met	Val	Thr	Ser	Asp	Gly	Lys	Val	Ile	Ser	Ser	Ala			
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Asp	Phe	His	Asn	Asp	Met	Lys	Thr	Pro	Ser	Ser	Phe	Asp	Lys	Val	Asp			
			-35						-30					-25				
Asp	Leu	Ser	Ser	Thr	Ile	Gly	Glu	Lys	Val	Lys	Pro	Leu	Thr	Thr	Tyr			
			-20					-15					-10					
Leu	Lys	Asp	Phe	Gln	Thr	Lys	Val	Val	Ile	Gly	Asp	Asp	Gly	Arg	Thr			
	-5					-1	1				5							

Sub B1

Lys Val Thr Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr Ile
10 15 20 25
Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn Lys
30 35 40
Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Thr Arg Ser Tyr
45 50 55
Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala Val
60 65 70
Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr Ile
75 80 85
Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp Thr
90 95 100 105
Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr Asn
110 115 120
Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys Met
125 130 135
Arg Ser Thr Gly Lys Val Ser Gln Trp Glu Met Ser Gly Pro Val Thr
140 145 150
Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Thr Ile Asp Thr Phe Ser Gly
155 160 165
Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly Val
170 175 180 185
His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys Ala
190 195 200
Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln
205 210 215

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<212> DNA
<213> Bacillus subtilis IS75

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<222> (280)..(939)

<220>
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<222> (1)..(102)
<223> pro-peptide (103) ... (279)

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gtt ttg tgt ttg gct ttg gca gca gcg gtt tct ttt ggc gta ccg gca 96

But 131

Val	Leu	Cys	Leu	Ala	Leu	Ala	Ala	Ala	Val	Ser	Phe	Gly	Val	Pro	Ala		
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Lys	Ala	Ala	Glu	Asn	Pro	Gln	Thr	Ser	Val	Ser	Asn	Thr	Gly	Lys	Glu		
	-60					-55				-50							
gct	gat	gct	acg	aaa	aac	caa	acg	tca	aaa	gca	gat	cag	gtt	tcc	gcc	192	
Ala	Asp	Ala	Thr	Lys	Asn	Gln	Thr	Ser	Lys	Ala	Asp	Gln	Val	Ser	Ala		
-45				-40						-35					-30		
cct	tat	gag	gga	acc	gga	aaa	aca	agt	aaa	tcg	tta	tac	ggc	ggc	caa	240	
Pro	Tyr	Glu	Gly	Thr	Gly	Lys	Thr	Ser	Lys	Ser	Leu	Tyr	Gly	Gly	Gln		
			-25						-20					-15			
acg	gaa	ctg	gaa	aaa	aac	att	caa	acc	tta	cag	cct	tcg	agc	att	atc	288	
Thr	Glu	Leu	Glu	Lys	Asn	Ile	Gln	Thr	Leu	Gln	Pro	Ser	Ser	Ile	Ile		
		-10					-5					-1	1				
gga	act	gat	gaa	cgc	acc	aga	atc	tcc	agc	acg	aca	tct	ttt	cca	tat	336	
Gly	Thr	Asp	Glu	Arg	Thr	Arg	Ile	Ser	Ser	Thr	Thr	Ser	Phe	Pro	Tyr		
	5					10					15						
aga	gca	acc	gtt	caa	ctg	tca	atc	aag	tat	ccc	aac	act	tca	agc	act	384	
Arg	Ala	Thr	Val	Gln	Leu	Ser	Ile	Lys	Tyr	Pro	Asn	Thr	Ser	Ser	Thr		
	20				25					30					35		
tat	gga	tgt	acc	gga	ttt	tta	gtc	aat	cca	aat	aca	gtc	gtc	acg	gct	432	
Tyr	Gly	Cys	Thr	Gly	Phe	Leu	Val	Asn	Pro	Asn	Thr	Val	Val	Thr	Ala		
				40					45					50			
gga	cat	tgt	gtg	tac	agc	cag	gat	cat	gga	tgg	gct	tcg	acg	ata	acc	480	
Gly	His	Cys	Val	Tyr	Ser	Gln	Asp	His	Gly	Trp	Ala	Ser	Thr	Ile	Thr		
			55				60						65				
gcc	gcg	ccg	ggc	cgc	aac	ggt	tcg	tca	tat	ccg	tac	ggt	act	tat	tca	528	
Ala	Ala	Pro	Gly	Arg	Asn	Gly	Ser	Ser	Tyr	Pro	Tyr	Gly	Thr	Tyr	Ser		
		70					75					80					
ggc	acg	atg	ttt	tac	tcc	gtc	aaa	gga	tgg	acg	gaa	agc	aaa	gac	acc	576	
Gly	Thr	Met	Phe	Tyr	Ser	Val	Lys	Gly	Trp	Thr	Glu	Ser	Lys	Asp	Thr		
	85					90					95						
aac	tat	gat	tac	gga	gct	att	aaa	tta	aac	ggt	tct	cct	gga	aac	acg	624	
Asn	Tyr	Asp	Tyr	Gly	Ala	Ile	Lys	Leu	Asn	Gly	Ser	Pro	Gly	Asn	Thr		
100					105					110					115		
gtt	ggc	tgg	tac	ggc	tac	cgg	act	aca	aac	agc	agc	agt	ccc	gtg	ggc	672	
Val	Gly	Trp	Tyr	Gly	Tyr	Arg	Thr	Thr	Asn	Ser	Ser	Ser	Pro	Val	Gly		
				120					125					130			
ctt	tcc	tcg	tca	gtg	aca	gga	ttc	cca	tgt	gac	aaa	acc	ttt	ggc	acg	720	
Leu	Ser	Ser	Ser	Val	Thr	Gly	Phe	Pro	Cys	Asp	Lys	Thr	Phe	Gly	Thr		
			135					140					145				
atg	tgg	tct	gat	aca	aag	ccg	att	cgc	tcc	gct	gaa	acg	tat	aag	ctg	768	
Met	Trp	Ser	Asp	Thr	Lys	Pro	Ile	Arg	Ser	Ala	Glu	Thr	Tyr	Lys	Leu		
		150					155					160					
acc	tat	aca	acc	gat	acg	tac	ggc	tgc	caa	agc	ggc	tcg	cct	gtt	tat	816	
Thr	Tyr	Thr	Thr	Asp	Thr	Tyr	Gly	Cys	Gln	Ser	Gly	Ser	Pro	Val	Tyr		
	165					170					175						
cga	aac	tac	agt	gat	aca	ggg	cag	aca	gct	att	gcc	att	cac	acc	aac	864	
Arg	Asn	Tyr	Ser	Asp	Thr	Gly	Gln	Thr	Ala	Ile	Ala	Ile	His	Thr	Asn		
180					185					190					195		

12-1-81

gga gga tcg tca tat aac ttg gga aca agg gtg acg aac gat gta ttc 912
Gly Gly Ser Ser Tyr Asn Leu Gly Thr Arg Val Thr Asn Asp Val Phe
200 205 210

aac aat att caa tat tgg gca aat caa 939
Asn Asn Ile Gln Tyr Trp Ala Asn Gln
215 220

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<213> Bacillus subtilis IS75

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-75 -70 -65

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-60 -55 -50

Ala Asp Ala Thr Lys Asn Gln Thr Ser Lys Ala Asp Gln Val Ser Ala
-45 -40 -35 -30

Pro Tyr Glu Gly Thr Gly Lys Thr Ser Lys Ser Leu Tyr Gly Gly Gln
-25 -20 -15

Thr Glu Leu Glu Lys Asn Ile Gln Thr Leu Gln Pro Ser Ser Ile Ile
-10 -5 -1 1

Gly Thr Asp Glu Arg Thr Arg Ile Ser Ser Thr Thr Ser Phe Pro Tyr
5 10 15

Arg Ala Thr Val Gln Leu Ser Ile Lys Tyr Pro Asn Thr Ser Ser Thr
20 25 30 35

Tyr Gly Cys Thr Gly Phe Leu Val Asn Pro Asn Thr Val Val Thr Ala
40 45 50

Gly His Cys Val Tyr Ser Gln Asp His Gly Trp Ala Ser Thr Ile Thr
55 60 65

Ala Ala Pro Gly Arg Asn Gly Ser Ser Tyr Pro Tyr Gly Thr Tyr Ser
70 75 80

Gly Thr Met Phe Tyr Ser Val Lys Gly Trp Thr Glu Ser Lys Asp Thr
85 90 95

Asn Tyr Asp Tyr Gly Ala Ile Lys Leu Asn Gly Ser Pro Gly Asn Thr
100 105 110 115

Val Gly Trp Tyr Gly Tyr Arg Thr Thr Asn Ser Ser Ser Pro Val Gly
120 125 130

Leu Ser Ser Ser Val Thr Gly Phe Pro Cys Asp Lys Thr Phe Gly Thr
135 140 145

Met Trp Ser Asp Thr Lys Pro Ile Arg Ser Ala Glu Thr Tyr Lys Leu
150 155 160

Thr Tyr Thr Thr Asp Thr Tyr Gly Cys Gln Ser Gly Ser Pro Val Tyr
165 170 175

But B1

Arg Asn Tyr Ser Asp Thr Gly Gln Thr Ala Ile Ala Ile His Thr Asn
180 185 190 195
Gly Gly Ser Ser Tyr Asn Leu Gly Thr Arg Val Thr Asn Asp Val Phe
200 205 210
Asn Asn Ile Gln Tyr Trp Ala Asn Gln
215 220

<210> 15
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Variation

<400> 15
Glu Lys Ala Ser
1

<210> 16
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Variation

<400> 16
Ser Glu Lys Ala Ser Thr
1 5

<210> 17
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Variation

<400> 17
Ser Glu Glu Thr
1

<210> 18
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> (1)..(38)
<223> n = A,T,C or G

<400> 18
ggatggagaa gcggaacac naaytaygay tayggngc

<210> 19
<211> 10

38

over 134

<212> PRT
<213> Artificial Sequence

<220>
<223> Variation

<400> 19
Gly Trp Arg Ser Gly Asn Tyr Asp Tyr Gly
1 5 10

<210> 20
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> 12,15
<223> n = deoxyInosine

<221> misc_feature
<222> 18,21 24
<223> n = A,T,C or G

<400> 20
cccaagcttg tngynacngc nggncayt

28

<210> 21
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Variation

<221> VARIANT
<222> 2<223> Xaa = Ala or Val

<400> 21
Val Xaa Thr Ala Gly His
1 5

<210> 22
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> (1)...(36)
<223> n = A,T,C or G

<400> 22
gaataccggt gaaccgcttt gncmncrta ngtrtc

36

<210> 23
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Variation

<221> VARIANT
<222> 5
<223> Xaa = Gly or Cys or Trp

<400> 23
Asp Thr Tyr Gly Xaa Gln Ser Gly Ser Pro Val Phe
1 5 10

<210> 24
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> (1)...(26)
<223> n = A,T,C or G

<400> 24
gctctagagt ydatngcncc rrtartc

26

<210> 25
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Variation

<221> VARIANT
<222> 6
<223> Xaa = Glu or Lys

<400> 25
Asp Tyr Gly Ala Ile Xaa
1 5

<210> 26
<211> 143
<212> DNA
<213> Bacillus

<400> 26
gcgtctatga cacggcaagc cgatcattcg cggaacccg caccgtttcc ccgggacgaa
acggttcagc ttacccttac ggatctgtta catcgaccgg ctatttcac cgcgcgggtt
ggcagagcgg aaattccaat tat

60
120
143

<210> 27
<211> 48
<212> PRT
<213> Bacillus

<400> 27
Cys Val Tyr Asp Thr Ala Ser Arg Ser Phe Ala Gly Thr Ala Thr Val
1 5 10 15
Ser Pro Gly Arg Asn Gly Ser Ala Tyr Pro Tyr Gly Ser Val Thr Ser
20 25 30
Thr Arg Tyr Phe Ile Pro Ser Gly Trp Gln Ser Gly Asn Ser Asn Tyr
35 40 45

Ref (3)

<210> 28
 <211> 184
 <212> DNA
 <213> Bacillus

<400> 28
 gatcgagctc agccagccga tcggcaatac cgtcggatat ttcggatatt catacaccgc 60
 ttcacgcgtt gcaggagcag gcgtgaccat cagcggatat ccaggagaca aaacaacagg 120
 caccagtggt gaaatgtccg gaacgatcgc tgtttcagaa acgtataaac tgcaatatgc 180
 gatc 184

<210> 29
 <211> 61
 <212> PRT
 <213> Bacillus

<400> 29
 Ile Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly Tyr
 1 5 10 15
 Ser Tyr Thr Ala Ser Ser Leu Ala Gly Ala Gly Val Thr Ile Ser Gly
 20 25 30
 Tyr Pro Gly Asp Lys Thr Thr Gly Thr Gln Trp Gln Met Ser Gly Thr
 35 40 45
 Ile Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile
 50 55 60

<210> 30
 <211> 143
 <212> DNA
 <213> Bacillus

<400> 30
 gcatttatga cacagcgagc gggtcattcg ccggaaccgc taccgtttct ccgggacgga 60
 acggttcaac atatccgtac ggatcagtta catcaaccgc ctatttcata ccgtcaggct 120
 atcgaagcgg aaattcgaat tac 143

<210> 31
 <211> 48
 <212> PRT
 <213> Bacillus

<400> 31
 Cys Ile Tyr Asp Thr Ala Ser Gly Ser Phe Ala Gly Thr Ala Thr Val
 1 5 10 15
 Ser Pro Gly Arg Asn Gly Ser Thr Tyr Pro Tyr Gly Ser Val Thr Ser
 20 25 30
 Thr Arg Tyr Phe Ile Pro Ser Gly Tyr Arg Ser Gly Asn Ser Asn Tyr
 35 40 45

<210> 32
 <211> 184
 <212> DNA
 <213> Bacillus

<400> 32
 catagagctc agccagccga tcggcaaacac cgtcgggtat ttcggatatt cctacaccac 60
 ctcgtctctc gttgggtcaa gcgttaccat catcggatat ccaggcgaca aaacatcggg 120
 cacccaatgg cagatgtccg gaaatatcgc cgtctcagaa acatataaac tgcaatatgc 180
 gatc 184

<210> 33
 <211> 61
 <212> PRT
 <213> Bacillus

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<400> 33
Ile Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly Tyr
1 5 10 15
Ser Tyr Thr Thr Ser Ser Leu Val Gly Ser Ser Val Thr Ile Ile Gly
20 25 30
Tyr Pro Gly Asp Lys Thr Ser Gly Thr Gln Trp Gln Met Ser Gly Asn
35 40 45
Ile Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile
50 55 60

<210> 34
<211> 19
<212> DNA
<213> Bacillus

<400> 34
cgtaagggta agctgaacc 19

<210> 35
<211> 23
<212> DNA
<213> Bacillus

<400> 35
caggagacaa aacaacagca ggc 23

<210> 36
<211> 18
<212> DNA
<213> Bacillus

<400> 36
gtccccggaga aacggtag 18

<210> 37
<211> 20
<212> DNA
<213> Bacillus

<400> 37
caccacctcg tctctcgttg 20

<210> 38
<211> 29
<212> DNA
<213> Bacillus

<220>
<221> misc_feature
<222> 18,21
<223> Xaa = deoxyInosine

<221> misc_feature
<222> 27
<223> n = A, G, C or T

<400> 38
gctctagacg tyttrtcncm nggrwancc 29

<210> 39
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Variation

221 VARIANT
222 2
223 Xaa = is Tyr or Phe

221 VARIANT
222 4
223 Xaa = is Gly or Cys

400 39
Gly Xaa Pro Xaa Asp Lys Thr
1 5

210 40
211 29
212 DNA
213 Artificial Sequence

220
223 Primer

221 misc_feature
222 12,15,21
223 n = is deoxyInosine

400 40
cccaagcttg tngtnathgg ngaygaygg

29

210 41
211 8
212 PRT
213 Artificial Sequence

220
223 Variation

400 41
Val Val Ile Gly Gly Asp Asp Gly
1 5

210 42
211 29
212 DNA
213 Artificial Sequence

220
223 Primer

400 42
gcacggaccg ttgcagttcg ttctggagc

29

210 43<211> 33
212 DNA
213 Artificial Sequence

220
223 Primer

400 43
cgggcaaagt gaatgaaaca aaggaaaaag cgg

33

210 44
211 31
212 DNA

12-1-85

<213> Artificial Sequence
<220>
<223> Primer

<221> misc_feature
<222> (1)..(31)
<223> n = A,T,C or G

<400> 44
atgcaccgga tggnnhatag gtccgaaaac c

<210> 45
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 45
ccctttaacc gcacaggtt t

31

21